

SEA 19

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 16:38:14 ; Search time 6.39535 Seconds
(without alignments)
142.679 Million cell updates/sec

Title: US-10-010-667A-19

Perfect score: 116
Sequence: 1 REV1HPLATSHQYFYKIPILV 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Sequences: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 116 | 100.0 | 339 | 1 STEA_HUMAN | Q9UHE8 homo sapien |
| 2 | 52.5 | 45.3 | 465 | 1 CIXG_HAETN | P44458 h cixg pro |
| 3 | 49 | 42.2 | 177 | 1 MSRA_HAETN | Q9H990 halobacteri |
| 4 | 47.5 | 40.9 | 320 | 1 CYE_FORPY | P51265 porphyra pu |
| 5 | 46 | 39.7 | 474 | 1 SYEA_ARATH | O9E034 arabidopsis |
| 6 | 46 | 39.7 | 737 | 1 YD27_MYCTU | O10638 mycobacteri |
| 7 | 46 | 39.7 | 1839 | 1 CYAA_SACLU | P23466 saccharomyc |
| 8 | 45 | 38.8 | 2549 | 1 FRAP_MOUSE | Q9J1N9 mus musculu |
| 9 | 44.5 | 38.4 | 137 | 1 SPWI_PIG | O8H112 methanosarc |
| 10 | 44.5 | 38.4 | 308 | 1 PYRB_METAC | P08266 diatomophila |
| 11 | 44.5 | 38.4 | 1176 | 1 RPB2_DROME | P48743 saccharomyc |
| 12 | 44 | 37.9 | 811 | 1 RPYL_YEAST | P14771 bovine hept |
| 13 | 44 | 37.9 | 928 | 1 VGLB_HSVB | P12640 bovine hept |
| 14 | 44 | 37.9 | 932 | 1 VGLB_HSVB | P33370 escherichia |
| 15 | 43.5 | 37.5 | 326 | 1 YJHS_ECOLI | P23247 vibrio chol |
| 16 | 43 | 37.1 | 337 | 1 DHAS_VIBCH | Q38913 arabidopsis |
| 17 | 43 | 37.1 | 373 | 1 EXTL_ARATH | O20701 caenorhabdi |
| 18 | 43 | 37.1 | 385 | 1 GBA5_CABEL | O30130 archaeoglob |
| 19 | 42.5 | 36.6 | 299 | 1 PYRB_ARCFU | Q9PCC4 xyliella fas |
| 20 | 42 | 36.2 | 216 | 1 MSRA_XYLEA | O60080 xyliella fas |
| 21 | 42 | 36.2 | 316 | 1 DHAS_VIBMT | P13267 bacillus su |
| 22 | 42 | 36.2 | 1437 | 1 DP03_BACSU | P43345 homo sapien |
| 23 | 42 | 36.2 | 2549 | 1 FRAP_HUMAN | P43346 rattus norv |
| 24 | 42 | 36.2 | 2549 | 1 FRAP_RAT | P24020 sus scrofa |
| 25 | 41.5 | 35.8 | 116 | 1 AON3_PIG | P02200 alligator m |
| 26 | 41.5 | 35.8 | 154 | 1 MYG_ALIMI | O92112 helicobacte |
| 27 | 41 | 35.3 | 196 | 1 COAE_HELPY | O25902 helicobacte |
| 28 | 41 | 35.3 | 196 | 1 COAE_HELPY | O25902 helicobacte |
| 29 | 41 | 35.3 | 576 | 1 SBP_CABEL | P75095 mycoplasma |
| 30 | 41 | 35.3 | 623 | 1 Y014_MYCPN | P26223 butyrivibri |
| 31 | 41 | 35.3 | 635 | 1 XINB_BOTFI | O85304 salmoneilla |
| 32 | 40.5 | 34.9 | 433 | 1 PEPD_SALDU | P25345 saccharomyc |
| 33 | 40.5 | 34.9 | 492 | 1 SYN1_YEAST | |

| | | | | | | |
|----|----|------|-----|---|------------|---------------------|
| 34 | 40 | 34.5 | 115 | 1 | GUAN_RAT | P28902 rattus norv |
| 35 | 40 | 34.5 | 246 | 1 | YU00_YEAST | P40165 saccharomyc |
| 36 | 40 | 34.5 | 317 | 1 | PLC_LISMO | P34024 listeria mo |
| 37 | 40 | 34.5 | 394 | 1 | NNN9_YEAST | P39107 saccharomyc |
| 38 | 40 | 34.5 | 526 | 1 | C11A_RAT | P14137 rattus norv |
| 39 | 40 | 34.5 | 625 | 1 | PARC_BORBU | O51066 borrelia bu |
| 40 | 40 | 34.5 | 695 | 1 | HRPI_PSEBY | P35655 pseudomonas |
| 41 | 40 | 34.5 | 868 | 1 | VGLB_VZVD | P03257 varicella-z |
| 42 | 40 | 34.5 | 870 | 1 | PLSB_XYLEA | Q9P077 xyliella fas |
| 43 | 40 | 34.5 | 903 | 1 | VGLB_HSVIF | P06436 herpes simp |
| 44 | 40 | 34.5 | 904 | 1 | VGLB_HSV11 | P10211 herpes simp |
| 45 | 40 | 34.5 | 904 | 1 | VGLB_HSV1K | P06437 herpes simp |

ALIGNMENTS

| RESULT 1 | ID | STEAD_HUMAN | STANDARD | PRT | 339 AA |
|----------|--|-----------------------------------|-----------|------------------|------------|
| AC | Q9UHE8 | O95034 | | | |
| DT | 16-OCT-2001 | (Rel. 40, Created) | | | |
| DT | 16-OCT-2001 | (Rel. 40, Last sequence update) | | | |
| DT | 15-JUN-2002 | (Rel. 41, Last annotation update) | | | |
| DE | Six transmembrane epithelial antigen of prostate. | | | | |
| DE | STEAP OR STEAP1. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. | | | | |
| OX | NCBI_Taxid=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=20056277; PubMed=10588738; | | | | |
| RA | Hubert R.S., Vivanco I., Chen E., Rastegar S., Leong K., | | | | |
| RA | Mitchell S.C., Madraswala R., Zhou Y., Kuo J., Raitano A.B., | | | | |
| RA | Jakovcic A., Saffran D.C., Afar D.E.H., | | | | |
| RT | "STEAP: a prostate-specific cell-surface antigen highly expressed in | | | | |
| RT | human prostate tumors."; | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 96:14523-14528(1999). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RA | Abu-Threideh J., Stoneking T., Langston Y., Maupin R.; | | | | |
| RL | Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases. | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Skin; | | | | |
| RA | Strausberg R.; | | | | |
| RL | Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases. | | | | |
| CC | -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential). | | | | |
| CC | -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PROSTATE TUMORS. | | | | |
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| CC | or send an email to license@sib-sib.ch). | | | | |
| CC | ----- | | | | |
| DR | EMBL; AF186249; AF17479.1; | | | | |
| DR | EMBL; AC005053; AAC79150.1; ALT_INT. | | | | |
| DR | EMBL; AC004969; AAD15620.1; ALT_INT. | | | | |
| DR | EMBL; BC011802; AAH1802.1; | | | | |
| DR | Genew; HGNC:11378; STEAP. | | | | |
| DR | MIM: 604415; | | | | |
| KM | Transmembrane; Antigen. | | | | |
| FT | TRANSMEM | 71 | | | POTENTIAL. |
| FT | TRANSMEM | 119 | | | POTENTIAL. |
| FT | TRANSMEM | 164 | | | POTENTIAL. |
| FT | TRANSMEM | 218 | | | POTENTIAL. |
| FT | TRANSMEM | 258 | | | POTENTIAL. |
| FT | TRANSMEM | 291 | | | POTENTIAL. |
| FT | SEQUENCE | 339 AA; | 39651 MW; | 55443AT10C870387 | CRC64; |

Query Match 100.0%; Score 116; DB 1; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2,5e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 REVHPLATSHQOYFYKIP 22
 Db 92 REVHPLATSHQOYFYKIP 113

RESULT 2
 CIXG_HAEIN STANDARD; PRT; 465 AA.

AC P4456;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE CIXG protein [includes: Apo-citrate lyase phosphoribosyl-dephospho-
 COA transferase (EC 2.7.7.-) (Apo-ACP nucleotidyltransferase); 2-(5'-
 dephosphoribosyl)-3'-dephosphocoenzyme-A synthase (EC 4.2.-.-) (2-
 5'-triphosphoribosyl)-3'-dephospho-CoA synthase].
 GN CIXG OR CIXG OR HI0021.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
 OC Haemophilus.
 OX NCBI_Taxid=727;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RC MEDLINE=95350630; PubMed=7542800;
 RA Fleischman R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shiley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips R., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fite L.D., Fitchman J.L., Furmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 Rd.";
 RL Science 269:496-512(1995).

CC -1- FUNCTION: BIFUNCTIONAL ENZYME THAT CATALYZES FORMATION OF 2-(5'-
 TRIPHOSPHORIBOSYL)-3'-DEPHOSPHOCOEZYME-A, AND THEN THE TRANSFER
 OF THIS PROSTHETIC GROUP PRECURSOR TO THE APO-ACTL CARRIER PROTEIN
 (GAMMA CHAIN) OF THE CITRATE LYASE TO YIELD THE HOLO-ACTL CARRIER
 PROTEIN (BY SIMILARITY).
 CC CATALYTIC ACTIVITY: Dephospho-CoA + ATP = 2-(5'-
 triphosphoribosyl)-3'-dephospho-CoA + adenine.
 CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE CIXG FAMILY.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE CIXG/MDCB
 FAMILY.

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 or send an email to license@isb-sib.ch).

CC EMBL; U32687; AAC21699.1; ALT_INIT.

DR TIGR; HI0021; -

DR InterPro; IPR002736; CIXG.

DR Pfam; PF01874; CIXG; 1.

KW Transferase; Nucleotidyltransferase; Lyase; Multifunctional enzyme;

KW Complete proteome.

FT DOMAIN 1 182 APO-CITRATE LYASE PHOSPHORIBOSYL-
 DEPHOSPHO-CoA TRANSFERASE.
 FT DOMAIN 183 465 2-(5'-TRIPHOSPHORIBOSYL)-3'-
 DEPHOSPHOCOEZYME-A SYNTHASE.

SEQUENCE 465 AA; 51834 MW; 4467221C3DB58A96 CRC64;

Query Match 45.3%; Score 52.5; DB 1; Length 465;
 Best Local Similarity 50.0%; Pred. No. 0.66;
 Matches 10; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy 1 REVHPLATSHQOYFYKIP 20
 Db 83 KEIRPLETGHAYFV-LPI 101

RESULT 3
 MSRA_HALNI STANDARD; PRT; 177 AA.

AC Q9H0G0;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peptide methionine sulfoxide reductase msra (EC 1.8.4.6) (Protein-
 methionine-S-oxide reductase) (peptide Met(O) reductase).
 GN MSRA OR VNG1180G.
 OS Halobacterium sp. (strain NRC-1).
 OC Archaea; Euryarchaeota; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_Taxid=64091;
 RN [1]

RP SEQUENCE FROM N.A.
 RC MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Shroga J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Weir R., Goo Y.A.,
 RA Leitauer B., Keller K., Cruz R., Danon M.J., Hough D.W., Dale H.,
 RA Maddock D.G., Jablonski P.E., Krebs M.P., Angvine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschoder M., Spudis J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Bhargava H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
 RT "Genome sequence of Halobacterium species NRC-1";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 CC -1- FUNCTION: Has an important function as a repair enzyme for
 proteins that have been inactivated by oxidation. Catalyzes the
 reversible oxidation-reduction of methionine sulfoxide in proteins
 to methionine (By similarity).

CC -1- CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin =
 protein L-methionine S-oxide + reduced thioredoxin.
 CC -1- SIMILARITY: BELONGS TO THE MSRA MET SULFOXIDE REDUCTASE FAMILY.
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CC EMBL; AB05045; MAG19555.1; -

DR HSP; P54149; LFA.

DR InterPro; IPR002569; PMSR.

DR Pfam; PF01625; PMSR; 1.

DR ProDom; PD003489; PMSR; 1.

DR TIGR; TIGR00401; msra; 1.

KW Oxidoreductase; Complete proteome.

FT ACT_SITE 12 12 BY SIMILARITY.

FT SEQUENCE 177 AA; 3378221C3DB58A96 CRC64;

Query Match 42.2%; Score 49; DB 1; Length 177;
 Best Local Similarity 50.0%; Pred. No. 0.81;
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 2 EVHPLATSHQOYFYKIP 19
 Db 135 ETVFAKQYFYKIP 152

RESULT 4
 CYP_FORPU

SEQ 20

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OM protein - protein search, using sw model

Run on: March 26, 2003, 16:38:14 / Search time 9.88372 Seconds
(without alignments)
142.679 Million cell updates/sec

Title: US-10-010-667A-20

Perfect score: 192
Sequence: 1 RRSYRYKLNMAYQVQVQNKEDAWIEHDVWRMEI 34

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Sequences: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|------------------------|
| 1 | 192 | 100.0 | 339 | 1 STEA_HUMAN | Q9ub68 homo sapien |
| 2 | 58.5 | 30.5 | 1418 | 1 CELL_CABEL | P34641 caenorhabd |
| 3 | 58 | 30.2 | 900 | 1 GAB_BACSU | P46918 bacillus su |
| 4 | 54 | 28.1 | 630 | 1 Y4BJ_RHISN | P55377 rhizobium su |
| 5 | 52 | 27.1 | 79 | 1 YOKC_BACSU | P54566 bacillus su |
| 6 | 52 | 27.1 | 1833 | 1 UN13_CABEL | P27715 caenorhabd |
| 7 | 51 | 26.6 | 495 | 1 GLPK_STY13 | P74260 synecocyst |
| 8 | 51 | 26.6 | 1017 | 1 ACAD_ARATN | Q91187 arabidopsis |
| 9 | 50 | 26.0 | 784 | 1 ALP4_SCHPO | Q91705 schizosacch |
| 10 | 50 | 26.0 | 1574 | 1 SYJ1_PAT | O62910 rattus norv |
| 11 | 50 | 26.0 | 5430 | 1 ACFF_HUMAN | O9upn3 homo sapien |
| 12 | 49.5 | 25.8 | 95 | 1 Y004_BACAN | O9rn28 bacillus an |
| 13 | 49.5 | 25.8 | 274 | 1 DAPD_BUCAT | P57323 buchnera ap |
| 14 | 49.5 | 25.8 | 350 | 1 YC73_METUA | O58669 methanococ |
| 15 | 49.5 | 25.8 | 940 | 1 SYV_CHLPS | Q92987 chlamydia p |
| 16 | 49 | 25.5 | 512 | 1 Y4WA_RHISN | P55679 rhizobium s |
| 17 | 49 | 25.5 | 837 | 1 NCM2_HUMAN | O15394 homo sapien |
| 18 | 49 | 25.5 | 837 | 1 NCM2_MOUSE | O35136 mus musculu |
| 19 | 49 | 25.5 | 1324 | 1 SYU1_BOVIN | O18964 bos taurus |
| 20 | 49 | 25.5 | 1575 | 1 SYU1_BOVIN | O43426 homo sapien |
| 21 | 48.5 | 25.3 | 266 | 1 IF2A_SUNSO | O97279 sulfolobus |
| 22 | 48.5 | 25.3 | 339 | 1 MOZL_CABEL | O92zm2 caenorhabd |
| 23 | 48 | 25.0 | 286 | 1 YAY8_SCHPO | O10216 schizosacch |
| 24 | 48 | 25.0 | 864 | 1 AGIU_MUGJA | O92442 muscivora javan |
| 25 | 48 | 25.0 | 942 | 1 ENV_CAEVG | P31637 caprine arc |
| 26 | 47.5 | 24.7 | 561 | 1 O16G_BACSU | O06994 bacillus su |
| 27 | 47.5 | 24.7 | 796 | 1 DHG_ECOLI | P15877 escherichia |
| 28 | 47.5 | 24.7 | 808 | 1 DHG_GLOX | P27175 glucosylact |
| 29 | 47.5 | 24.7 | 1103 | 1 CYGF_BOVIN | O02740 bos taurus |
| 30 | 47 | 24.5 | 244 | 1 CYBH_BRAJA | P19660 bradyrhizob |
| 31 | 47 | 24.5 | 586 | 1 VATA_HALVO | O48332 halobacteri |
| 32 | 47 | 24.5 | 675 | 1 VPS5_YEAST | O92331 saccharomyc |
| 33 | 47 | 24.5 | 1002 | 1 POL_HV1U4 | P24740 human immun |

| | | | | | |
|----|------|------|------|--------------|--------------------|
| 34 | 47 | 24.5 | 1133 | 1 ATX9_TETTH | O95050 tetrahymena |
| 35 | 47 | 24.5 | 1503 | 1 TRL2_HUMAN | O94759 homo sapien |
| 36 | 46.5 | 24.2 | 215 | 1 CIB2_HUMAN | O60939 homo sapien |
| 37 | 46.5 | 24.2 | 215 | 1 CIB2_RAT | P54900 rattus norv |
| 38 | 46.5 | 24.2 | 463 | 1 SYN_GLOAB | O9766 clostridium |
| 39 | 46.5 | 24.2 | 508 | 1 O16G_BACSP | P29093 bacillus sp |
| 40 | 46.5 | 24.2 | 555 | 1 O16G_BACCO | O45101 bacillus co |
| 41 | 46 | 24.0 | 220 | 1 DIB7_MOUSE | O9qy18 mus musculu |
| 42 | 46 | 24.0 | 236 | 1 BIR8_GORGO | O95m71 gorilla gor |
| 43 | 46 | 24.0 | 236 | 1 BIR8_HUMAN | O96p09 homo sapien |
| 44 | 46 | 24.0 | 236 | 1 BIR8_PANTR | O95m72 pan troglod |
| 45 | 46 | 24.0 | 242 | 1 DIB6_MOUSE | O54946 mus musculu |

ALIGNMENTS

| RESULT 1 | ID | STANDARD | PRT | 339 AA. |
|----------|--|----------|-----|------------|
| AC | Q9UHE8; 095034; | | | |
| DT | 16-OCT-2001 (Rel. 40, Created) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | |
| DT | 15-JUN-2002 (Rel. 41, Last annotation update) | | | |
| DE | Six transmembrane epithelial antigen of prostate. | | | |
| OS | STEAP OR STEAP1. | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | |
| OX | NCBI_Taxid=9606; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=20056277; PubMed=10588738; | | | |
| RA | Hubert R.S., Vivanco I., Chen E., Raetegar S., Leong K., | | | |
| RA | Mitchell S.C., Madraswala R., Zhou Y., Kuo J., Raitano A.B., | | | |
| RA | Jakobovits A., Saffran D.C., Afar D.E.H.; antigen highly expressed in | | | |
| RT | "STEAP: a prostate-specific cell-surface antigen highly expressed in | | | |
| RT | human prostate tumors."; | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 96:14523-14528 (1999). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Abu-Threideh J., Stoneking T., Langston Y., Maupin R.; | | | |
| RL | Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases. | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Skin; | | | |
| RA | Strausberg R.; | | | |
| RL | Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases. | | | |
| CC | -1- SUBCELLULAR LOCATION: Integral membrane protein (potential). | | | |
| CC | -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PROSTATE TUMORS. | | | |
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| CC | | | | |
| DR | EMBL; AF186249; AA017479.1; - | | | |
| DR | EMBL; AC005053; AAC79150.1; ALT_INIT. | | | |
| DR | EMBL; AC004969; AAD15620.1; ALT_INIT. | | | |
| DR | EMBL; BC011802; AAH11802.1; - | | | |
| DR | Gene; HGNC:11378; STEAP. | | | |
| DR | MM; 604415; - | | | |
| KM | Transmembrane; Antigen. | | | |
| FT | TRANSMEM 71 91 | | | POTENTIAL. |
| FT | TRANSMEM 119 139 | | | POTENTIAL. |
| FT | TRANSMEM 164 184 | | | POTENTIAL. |
| FT | TRANSMEM 218 238 | | | POTENTIAL. |
| FT | TRANSMEM 258 278 | | | POTENTIAL. |
| FT | TRANSMEM 291 311 | | | POTENTIAL. |
| SO | SEQUENCE 339 AA; 39851 MW; 55443A170C870387 CRC64; | | | |

Query Match 100.0%; Score 192; DB 1; Length 339;
 Best Local Similarity 100.0%; Pred. No. 9,4e-19;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRSRYKLTNMAVQVQONKEDAMIEHDVWMEI 34
 DB 185 RRSRYKLTNMAVQVQONKEDAMIEHDVWMEI 218

RESULT 2

CE11 CAEEL STANDARD; PRT; 1418 AA.
 AC P34611;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ccd-11 protein.
 GN F011 OR ZK512.3.
 OS Rhabditidae; Elenegans.
 CC Rhabditidae; Elenegans.
 CC Rhabditidae; Pelodierinae; Caenorhabditis.
 CC NCBI_TaxID=6239;

SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RC MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Cratford M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kersey J., Kirschen J., Laister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Riken L., Roop A., Saunders D., Shownkeen R.,
 RA Sims M., Smalton N., Smith A., Smith K., Staden E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston J., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Wodhams P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).

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DR EMBL; Z22177; CA80145.1;
 DR PIR; S40764; S40764;
 DR WormPep; ZK512.3; CE00409;
 DR InterPro; IPR002111; Cat_channel_TPL.
 SQ SEQUENCE 1418 AA; 159237 MW; 4FC83B9E7ADF7788 CRC64;

Query Match 30.5%; Score 58.5; DB 1; Length 1418;
 Best Local Similarity 43.5%; Pred. No. 5.2;
 Matches 10; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

QY 15 OYQONKED--AMIEHDVWMEI 34
 DB 1355 EVAENEDTDMNATHEHDVWMAISL 1377

RESULT 3
 GAB_BACSU STANDARD; PRT; 900 AA.
 AC P46918;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Minor teichoic acids biosynthesis protein g9ab.

QY 2 RSRRYKLTNMAVQVQONKEDAMIEHDVWMEI 34
 DB 591 RSRRYKLTNMAVQVQONKEDAMIEHDVWMEI 623

GN GAB.
 OS Bacillus subtilis.
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CC NCBI_TaxID=1423;

QY 15 OYQONKED--AMIEHDVWMEI 34
 DB 1355 EVAENEDTDMNATHEHDVWMAISL 1377

SEQUENCE FROM N.A.

RC STRAIN=168;
 RC MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertsche M.G., Bessieres P., Borchert S., Bron S.,
 RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Dentzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Enrian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Kleeer-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidis A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Portolillo S., Prescott A.M.,
 RA Plesch E., Pucic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
 RA Sekiguchi J., Sekowska A., Serr S.J., Serr P., Shin B.S., Soldo B.,
 RA Sorokin A., Taconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
 RA Tostato V., Uchiyama S., Vandenberg M., Vannier F., Vassarotti A.,
 RA Viari A., Wandut R., Wedler E., Wedler H., Weitenegger T.,
 RA Winers P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis.";
 RL Nature 390:249-256(1997).

CC FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF GALACTOSAMINE-CONTAINING
 CC MINOR TEICHOIC ACIDS.

CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
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DR EMBL; U13979; AAA73513.1;
 DR EMBL; Z99122; CAB15585.1;
 DR Subtilast; BG11192; g9ab.
 DR InterPro; IPR001173; Glycos_transf_2.
 DR Pfam; PF00535; Glycos_transf_2; 1.
 KV Transferrase; Glycosyltransferase; Complete proteome.
 SQ SEQUENCE 900 AA; 107154 MW; FA66495486C2C6F CRC64;

Query Match 30.2%; Score 58; DB 1; Length 900;
 Best Local Similarity 33.3%; Pred. No. 3.7;
 Matches 11; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 2 RSRRYKLTNMAVQVQONKEDAMIEHDVWMEI 34
 DB 591 RSRRYKLTNMAVQVQONKEDAMIEHDVWMEI 623

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 16:38:14 ; Search time 4.36047 Seconds
(without alignments)
142.679 Million cell updates/sec

Title: US-10-010-667A-21
Perfect score: 93
Sequence: 1 WIDIKQFVWYPTPTF 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Sequences: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.+

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 93 | 100.0 | 339 | 1 STEA_HUMAN | Q9ubh8 homo sapien |
| 2 | 53 | 55.9 | 458 | 1 AGLE_RHIME | Q9z3t5 rhizobium m |
| 3 | 45 | 48.4 | 865 | 1 ENV_HV1RH | P04579 human immun |
| 4 | 43.5 | 46.8 | 1167 | 1 WCI_NEUCR | Q01371 neuropeptid |
| 5 | 42 | 45.2 | 346 | 1 OPRF_ICTPU | P42266 ictalurus p |
| 6 | 42 | 45.2 | 396 | 1 YUR1_YEAST | P46992 saccharomyc |
| 7 | 42 | 45.2 | 685 | 1 ERP2_YEAST | P05453 saccharomyc |
| 8 | 42 | 45.2 | 795 | 1 TLR1_MOUSE | Q9epd1 mus musculu |
| 9 | 42 | 45.2 | 847 | 1 ENV_HV1S1 | P19550 human immun |
| 10 | 41.5 | 44.6 | 224 | 1 YN89_YEAST | P53721 saccharomyc |
| 11 | 41 | 44.1 | 405 | 1 WCAD_ECOLI | P12328 escherichia |
| 12 | 41 | 44.1 | 430 | 1 PUCK_BACSU | O32140 bacillus su |
| 13 | 41 | 44.1 | 703 | 1 ARPB_MANSE | P14227 manduca sex |
| 14 | 41 | 44.1 | 843 | 1 ENV_HV1Y2 | P35961 human immun |
| 15 | 41 | 44.1 | 854 | 1 ENV_SIVZ2 | P17281 chimpanzee |
| 16 | 41 | 44.1 | 856 | 1 ENV_HV1Z8 | P05821 human immun |
| 17 | 41 | 44.1 | 1509 | 1 MYSN_ACACA | P05659 acanthamoeb |
| 18 | 41 | 44.1 | 1628 | 1 NAGH_CLOPE | P26831 clostridium |
| 19 | 40 | 43.0 | 226 | 1 HAP2_RABIT | P20755 crytocolagus |
| 20 | 40 | 43.0 | 847 | 1 ENV_HV1Y2 | P05860 human immun |
| 21 | 40 | 43.0 | 853 | 1 ENV_HV1Z2 | P12487 human immun |
| 22 | 40 | 43.0 | 855 | 1 ENV_HV1Z6 | P04580 human immun |
| 23 | 40 | 43.0 | 856 | 1 ENV_HV1N6 | P05877 human immun |
| 24 | 39.5 | 42.5 | 263 | 1 MPPI_LOLPR | P14946 lolium pere |
| 25 | 39.5 | 42.5 | 263 | 1 MPPI_PHLPR | P43223 phleum prat |
| 26 | 39.5 | 42.5 | 265 | 1 MPPI_HOILA | P43216 holcus lana |
| 27 | 39.5 | 42.5 | 269 | 1 MPPI_PHAHQ | Q41260 phalaris aq |
| 28 | 39.5 | 42.5 | 551 | 1 YABN_ECOLI | P33595 escherichia |
| 29 | 39.5 | 42.5 | 701 | 1 ACSA_HUMAN | O9nri9 homo sapien |
| 30 | 39 | 41.9 | 210 | 1 SSH5_YEAST | O03446 saccharomyc |
| 31 | 39 | 41.9 | 223 | 1 CDRI_HUMAN | P31861 homo sapien |
| 32 | 39 | 41.9 | 282 | 1 Y765_HABIN | Q57145 haemophilus |
| 33 | 39 | 41.9 | 289 | 1 MTM3_METUA | Q58015 methanococc |

| | | | | | |
|----|------|------|-----|--------------|---------------------|
| 34 | 39 | 41.9 | 361 | 1 SERC_BACHD | Q9kdm4 bacillus ha |
| 35 | 39 | 41.9 | 459 | 1 NUAM_MACRO | P92668 macropus ro |
| 36 | 39 | 41.9 | 847 | 1 MDOH_ECOLI | P33137 escherichia |
| 37 | 39 | 41.9 | 853 | 1 ENV_HV1EL | P04581 human immun |
| 38 | 39 | 41.9 | 868 | 1 ENV_HV1C4 | P05879 human immun |
| 39 | 38.5 | 41.4 | 614 | 1 YEHQ_ECOLI | P33353 escherichia |
| 40 | 38 | 40.9 | 258 | 1 RCEH_RHOVI | P06008 rhodospheuo |
| 41 | 38 | 40.9 | 330 | 1 HEM2_AOUAE | O67876 aquiflex aeo |
| 42 | 38 | 40.9 | 566 | 1 MBHM_ECOLI | P37181 escherichia |
| 43 | 38 | 40.9 | 702 | 1 DDHX_MOUSE | O61496 mus musculu |
| 44 | 38 | 40.9 | 707 | 1 JIP1_MOUSE | O9evr19 mus musculu |
| 45 | 38 | 40.9 | 708 | 1 JIP1_RAT | Q9t237 r c-jun-am1 |

ALIGNMENTS

| RESULT 1 | ID | STEA_HUMAN | STANDARD; | PRT; | 339 AA. |
|----------|--|------------|-----------|------|------------|
| AC | Q9UEB8; Q95034; | | | | |
| DT | 16-OCT-2001 (Rel. 40, Created) | | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | | |
| DT | 15-JUN-2002 (Rel. 41, Last annotation update) | | | | |
| DE | Six transmembrane epithelial antigen of prostate. | | | | |
| GN | STEAP OR STEAP1. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=20056277; PubMed=10586738; | | | | |
| RA | Hubert R.S., Vivanco I., Chen E., Rastegar S., Leong K., | | | | |
| RA | Mitchell S.C., Madraswala R., Zhou Y., Kuo J., Raitano A.B., | | | | |
| RA | Jakobovits A., Salfran D.C., Afar D.E.H.; | | | | |
| RT | "STEAP: a prostate-specific cell-surface antigen highly expressed in | | | | |
| RT | human prostate tumors."; | | | | |
| RT | Proc. Natl. Acad. Sci. U.S.A. 96:14523-14528(1999). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RA | Abu-Threideh J., Stoneking T., Langston Y., Maupin R.; | | | | |
| RL | Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases. | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | Strausberg R.; | | | | |
| RA | Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases. | | | | |
| RL | Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases. | | | | |
| CC | -1- SUBCELLULAR LOCATION: Integral membrane protein (potential). | | | | |
| CC | -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PROSTATE TUMORS. | | | | |
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| CC | ----- | | | | |
| EMBL: | A186249; AAF17479.1; - | | | | |
| DR | EMBL; AC005053; AAC79150.1; ALT_INIT. | | | | |
| DR | EMBL; AC004969; AAD15620.1; ALT_INIT. | | | | |
| DR | EMBL; BC011802; AAH11802.1; - | | | | |
| DR | Gene; HGNC:11378; STEAP. | | | | |
| DR | MIM; 604415; - | | | | |
| KW | Transmembrane; Antigen. | | | | |
| FT | TRANSMEM 71 91 | | | | POTENTIAL. |
| FT | TRANSMEM 119 139 | | | | POTENTIAL. |
| FT | TRANSMEM 164 184 | | | | POTENTIAL. |
| FT | TRANSMEM 218 238 | | | | POTENTIAL. |
| FT | TRANSMEM 258 278 | | | | POTENTIAL. |
| FT | TRANSMEM 291 311 | | | | POTENTIAL. |
| FT | SEQUENCE 339 AA; 39851 MW; 55443A170C870387 CRC64; | | | | |

